

SFQ ID NO.1FIG.1 a

GAATTCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(UPPER:SEQ ID NO.1)
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCAATGTAGACAT	119 39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179 59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTTATTTATGCACAGGGTGGAACAAG	239 79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299 99
MDYQVSSPIYDINYYTSEPC	
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359
QKINVKQIAARLLPPLYSLV	119
TTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG	419 139
FIFFGVGNMLVILILINCKR	
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479 159
LKSMTDIYLLNLALISDLFFL	
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539 179
LTVPFWAHYAAAQWDFGNMTM	
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599 199
CQLLTGLYFIFGFFSGIFFI	
CTCCTGACAATCGATAGGTACCTGGCTGTCTGTCATGCTGTGTTTGCTTTAAAAGCCAGG	659 219
LLTDRLYLAVVHA VFA LKAR	
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT	719 239
TVTFGVVTSVITWVVAVFAS	
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779 259
LPGIIFTRSQKEGLHYTCS	
CATTTTCCATACA	
HFPY	

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59(UPPER:SEQ ID NO.2)
	19(LOWER:SEQ ID NO.5)
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT	119
	39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTATGCACAGGGTGGAACAAG	239
	79
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99
CAAAAAATCAATGTGAAGCAAATCGCAGCCCCGCTCCTGCCTCCGCTCTACTCACTGGTG	359
Q K I N V K Q I A A R L L P P L Y S L V	119
TTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAGG	419
I F G F V G N M L V I L I L I N C K R	139
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479
L K S M T D I Y L L N L A I S D L F F L	159
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539
T V P F W A H Y A A A Q W D F G N T M	179
TTTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599
Q L L T G L Y F I G F F S G I F F I I	199
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659
L L T I D R Y L A V V H A V F A L K A R	219
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCGTCT	719
T V T F G V V T S V I T W V V A V F A S	239
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779
L P G I I F T R S Q K E G L H Y T C S S	259
CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC	839
H F P Y S Q Y Q F W K N F Q T L K I V I	279

SEQ ID NO.2 FIG.1b

TTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGGAATCCTAAAACT 899
L G L V L P L L V M V I C Y S G I L K T 299

CTGCTTCGGTGTGCGAAATGAGAAGAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC 959
L L R C R N E K K R H R A V R L I F T I 319

ATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACATTGTCTTCTCCTGAACACCTTC 1019
M I V Y F L F W A P Y N I V L L L N T F 339

CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTTGGACCAAGCTATGCAG 1079
Q E F F G L N N C S S S N R L D Q A M Q 359

GTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCCATCATCTATGCCTTTGTC 1139
V T E T L G M T H C C I N P I I Y A F V 379

GGGGAGAAGTTTCAGAACTACCTCTTAGTCTTCTTCCAAAAGCACATTGCCAAACGCTTC 1199
G E K F R N Y L L V F F Q K H I A K R F 399

TGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1259
C K C C S I F Q Q E A P E R A S S V Y T 419

CGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT 1319
R S T G E Q E I S V G L * 439

GAGGCAGTCAGAGTTGTGCACATGGCTTAGTTTTTCATACACAGCCTGGGCTGGGGGTNGG 1379
459

TTGGNNGAGGTCTTTTTTAAAAGGAAGTTACTGTTATAGAGGGTCTAAGATTCATCCATT 1439
479

TATTTGGCATCTGTTTAAAGTAGATTAGATCCGAATTC

SEQ ID NO.2 (SUITE)

FIG.1c

GAATTCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59	UPPER: SEQ ID NO. 3
	19	LOWER: SEQ ID NO. 6
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAAGAGAGTTAATTCATGTAGACAT	119	
	39	
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCATTCATGGAGGGCAAC	179	
	59	
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTTATTTATGCACAGGGTGAACAAG	239	
	79	
ATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299	
M D Y Q V S S P I Y D I N Y Y T S E P C	99	
CAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG	359	
Q K I N V K Q I A A R L L P P L Y S L V	119	
TTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAGG	419	
F I F G F V G N M L V I L I L I N C K R	139	
CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT	479	
L K S M T D I Y L L N L A I S D L F F L	159	
CTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG	539	
F T V P F W A H Y A A A Q W D F G N T M	179	
TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC	599	
E Q L L T G L Y F I G F F S G I F F I I	199	
CTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATGCTGTGTTTGCTTTAAAAGCCAGG	659	
L L T I D R Y L A V V H A V F A L K A R	219	
ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGCCTCT	719	
T V T F G V V T S V I T W V V A V F A S	239	
CTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTTCATTACACCTGCAGCTCT	779	
L P G I I F T R S Q K E G L H Y T C S S	259	
CATTTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGT	839	
H F P Y I K D S H L G A G P A A A C H G	279	

SEQ ID NO.3FIG.1d

CATCTGCTACTCGGGAATCCTAAAACTCTGCTTCGGTGTGCGAAATGAGAAGAAGAGGCA	899
H L L L G N P K N S A S V S K *	299
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTA	959
	319
CAACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019
	339
CTCTAACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079
	359
CATCAACCCCATCATCTATGCCTTTGTGCGGGGAGAAGTTCAGAACTACCTCTTAGTCTT	1139
	379
CTTCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199
	399
TCCCAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGG	1259
	419
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319
	439
TTGATACACAGCCTGGGCTGGGGGTNGGTTGGNNGAGGTCTTTTTTAAAAGGAAGTTACT	1379
	459
GTATAGAGGGTCTAAGATTCATCCATTTATTTGGCATCTGTTTAAAGTAGATTAGATCC	1439
	479
GAATTC	

SEQ ID NO.3 (SUITE)

FIG.1e

FIG. 2

I		II	
CCR5	1 M Y Q V S S P I D I N Y T S E P C Q K I N V K Q I A R I L P P L Y S I V F I F G E V G N M L V I L I N C K R L K S M T D I Y L I N I A I S D I F I T	83	
HCC-R2b	MLSTSRSRFTRN'NESGEEVTTFTFYDYGAPOHFTYKQI L A Q I I P P L Y S I V F I F G E V G N M L V I L I N C K K I K C I P D I Y L L N I A I S D I F I T	95	
HCC-R3	MTTSI I V E T F G T S Y D D V G L I E K A D T R A L M A Q F V P P L Y S I V F I F G E V G N M L V I L I N C K K I K Y R R I R I M T I Y L L N I A I S D I F I T	8	
HCC-R1	METPNTT E D Y D T T E F I Y G D A T P C Q K V N E R A F G P Q L L P P L Y S I V F I F G E V G N I L V V I V Q Y K R L K N M T S I Y L L N I A I S D I F I T	87	
HCC-R4	MNPTDIADTLD E S I Y S N I Y L Y E S I P K P C I K E G I K A F G E L I L P P L Y S I V F I F G E V G N M L V I L I N C K R I R S M T D I Y L L N I A I S D I F I T	92	
III		IV	
CCR5	V P F W A H Y A P A Q W D F G N I M C Q L L T G I X F I G F F S G I F F I I L I T I D R Y I A M V H A V F A I K A R T V T F G V V T S V I T W V A V F A S L P G I I F T R Q K E G I	177	
HCC-R2b	I P I W A H I A P A N E M V F G N A M C K I F T G L Y I I G F F I G I F F I I L I T I D R Y I A I V H A V F A I K A R T V T F G V V T S V I T W V A V F A S L P G I I F T R Q K E I D S V	189	
HCC-R3	I P F W I I Y V R G I N W F C H I C M C N L I E G F Y I T C L Y S E I F F I I L I T I D R Y I A I V H A V F A I R A R T V T F G V I T F I V T W G I A M A R I L E R I F Y E T F E L F E E	182	
HCC-R1	I P F W I I Y K I K D I W F G D A M C K I L S G F Y T G L Y S E I F F I I L I T I D R Y I A I V H A V F A I R A R T V T F G V I T S I I W A I A I I A S M P C L Y F S K T W E F T I	182	
HCC-R4	I P F W G Y Y A A I Q W V E G L G I C K M I S W M Y L V G F Y S G I F F I F V M M S I D R Y I A I V H A V F A I R A R T I I Y G V I T S L A T W S V A V F A S L P G I I E S T C Y T E R N E	186	
V		VI	
CCR5	Y T C S I H E P Y S Q Y Q F W K N F Q T L K T V I L G L V L P L I A M V I C Y S G T L K T I L R C R N E K K R I R A V R L I F T I M I V Y F L E W A P Y N I V L L I N T F Q E F F G L N N C	272	
HCC-R2b	M G I Y P T A G . . . W N E I I T M R N I L G L V L P L I I M V T C Y S G T L K T I L R C R N E K K R I R A V R V I F T I M I V Y F L E W P P Y N I V I L I N T F Q E F F G L N N C	280	
HCC-R3	T I I A L Y E D T V Y S W R H E I T R M T I F C I V I P L I A M I C Y I G I I K T I L R C P E K K Y K A I I I F V I M A V F I F W P P Y N V A I I I S S Y I S I I F C I	27	
HCC-R1	I T C S I H E P H E S L R E W K L F C A L K L N L F G L V L P L I A M I C Y I G I I K I L L R R P N E K K S K A V R I I F V I M I I F F L E W P P Y N L T I I I S V F Q E F L E T H E C	276	
HCC-R4	T Y C K T K Y S I N S T I W K V L S S E I N I L G L V I P I G I M I F C Y S M I R T L Q H K N E K K N K A V K M I E A V V V L F L G F W P P Y N I V I F I E T L V E L E V I Q D C	279	
VII		VIII	
CCR5	S S I N R I D Q A M Q V T E T L G M T H C C I N P I I Y A F V G E K F R N Y I L L V F E C K I I T A K R F C K C S I F C L E A I E R A S S V Y I K S T G E Q E I S M G I	352	
HCC-R2b	F P I S Q I D Q A I Q V T E T L G M T H C C I N P I I Y A F V G E K F R Y I S V F F K K I I I F C K I C P V E T K P V D G V T I T N I F S T G E Q E N S A G I	360	
HCC-R3	E R I K H I I D V I V T E V T A Y S H C C N H I V I Y A F V G E I R K Y I R H E F H I I I I M I I G R Y I P E L I E R I S S V I E R I S I V F	355	
HCC-R1	E L E K H I I D A M Q V T E V I A Y T H C C V N I V I Y A F V G E I R K Y I R Q I E R R V A V I I I M I P F L S V D R I E R V S T S I S T G E I I S A C I	355	
HCC-R4	T F E R Y L D V A I Q A T E T L A F V H C C I N P I I Y I F E I G E K F R K Y I I Q L E K G L F V I Q Y Q G L I Q I Y S A D T H S S Y T Q S T M D H D L H D A I	360	

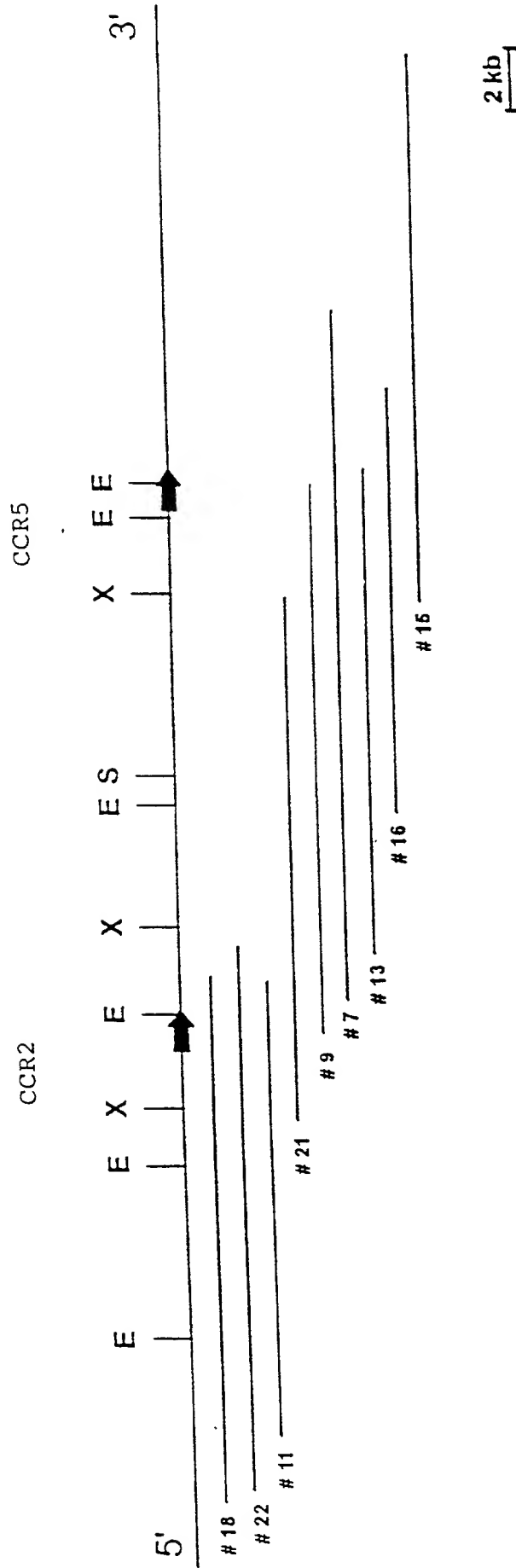


FIG. 3

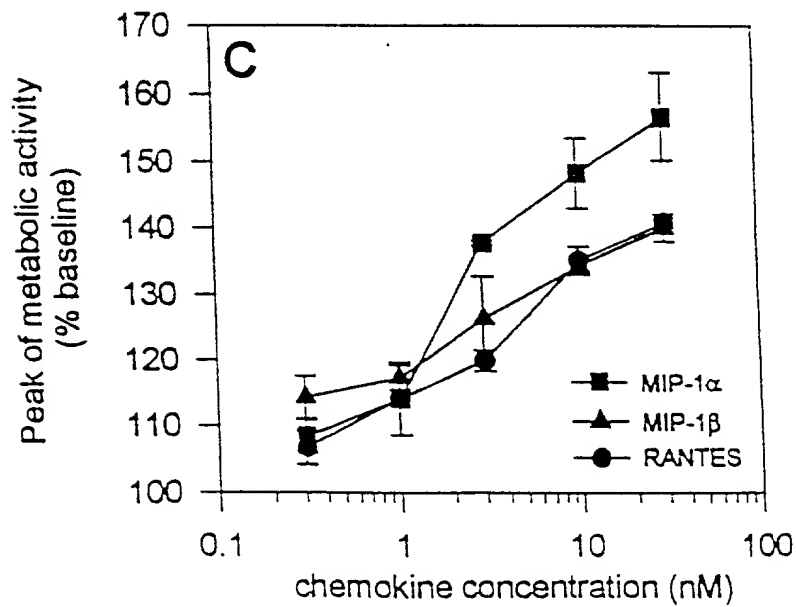
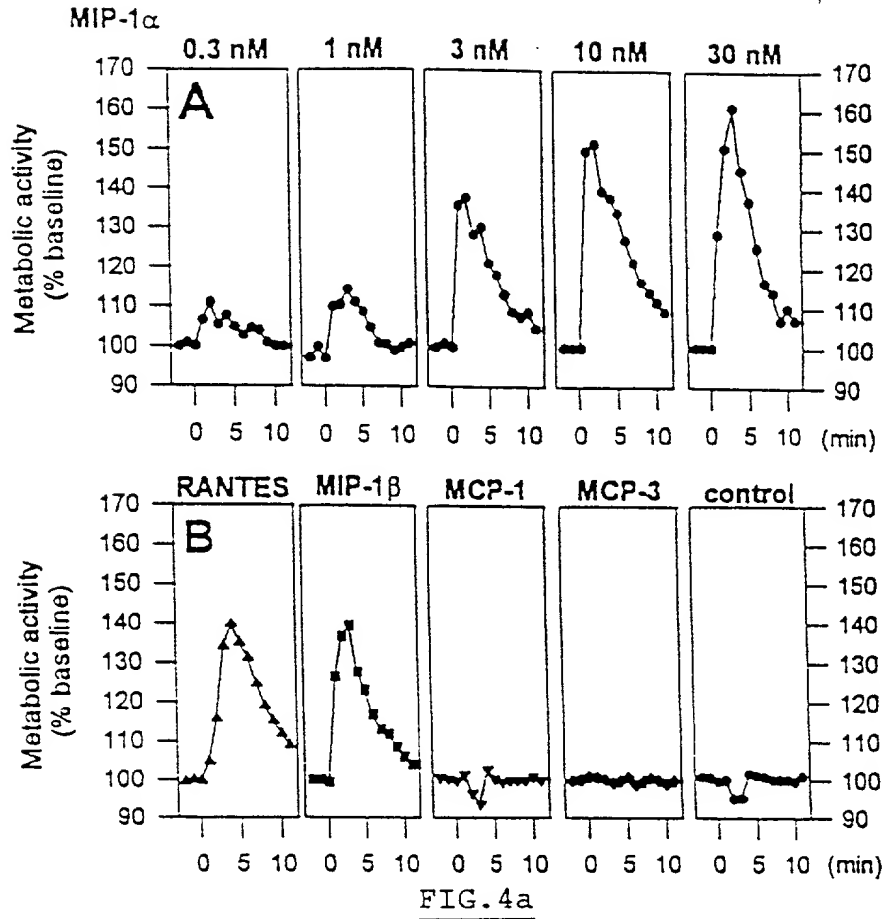


FIG. 4b

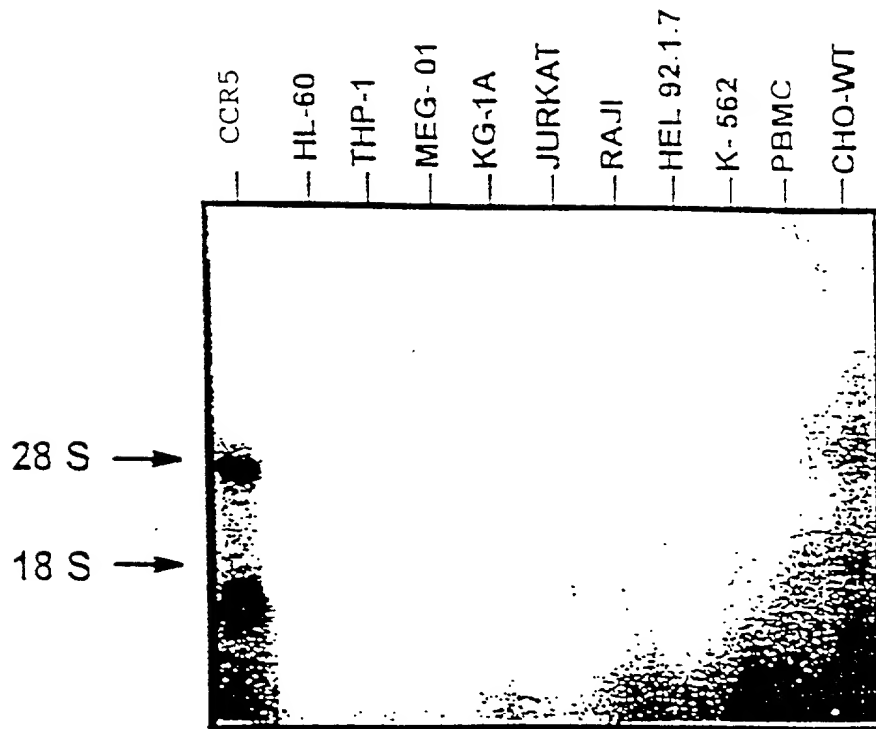


FIG. 5

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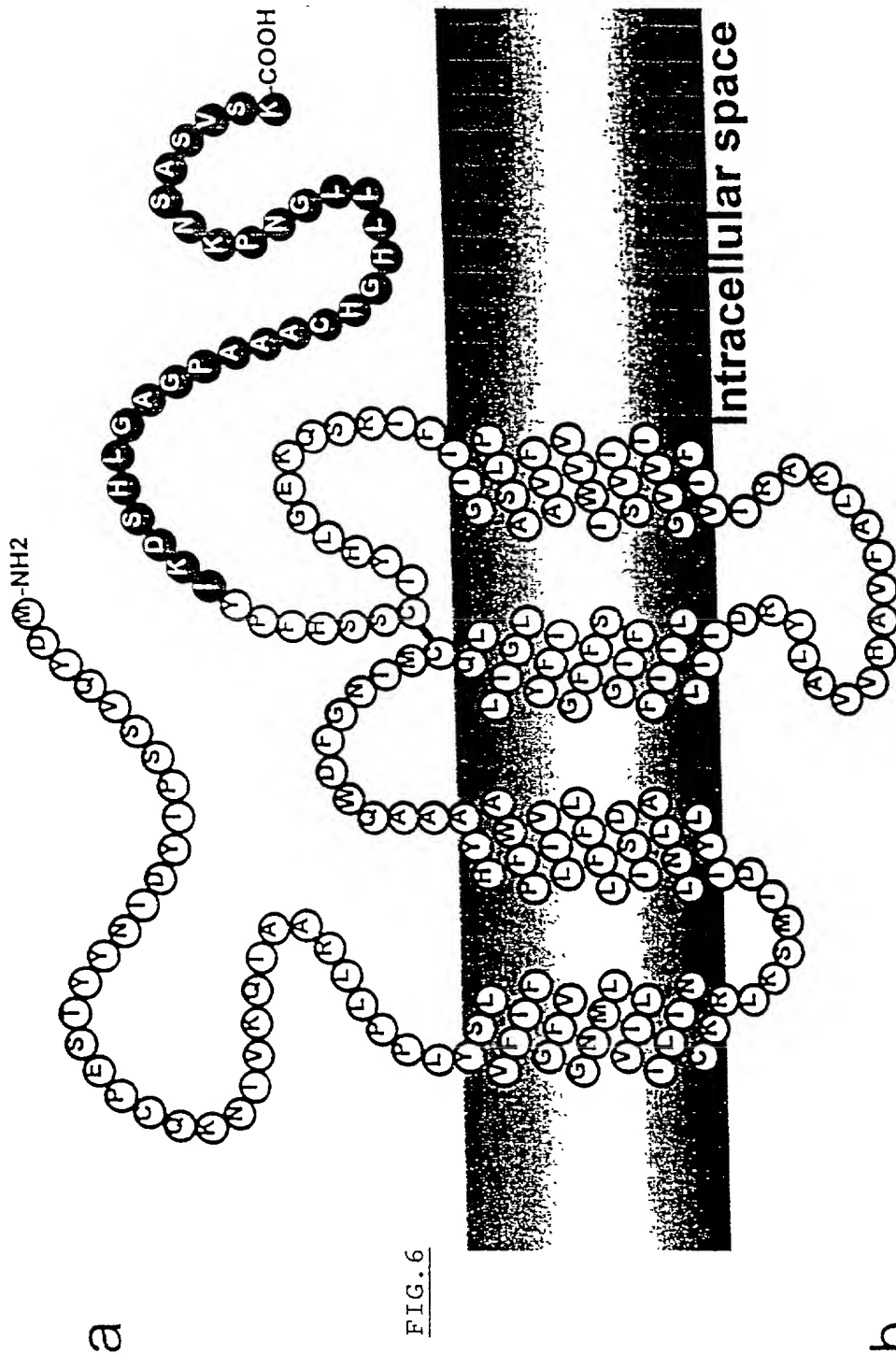
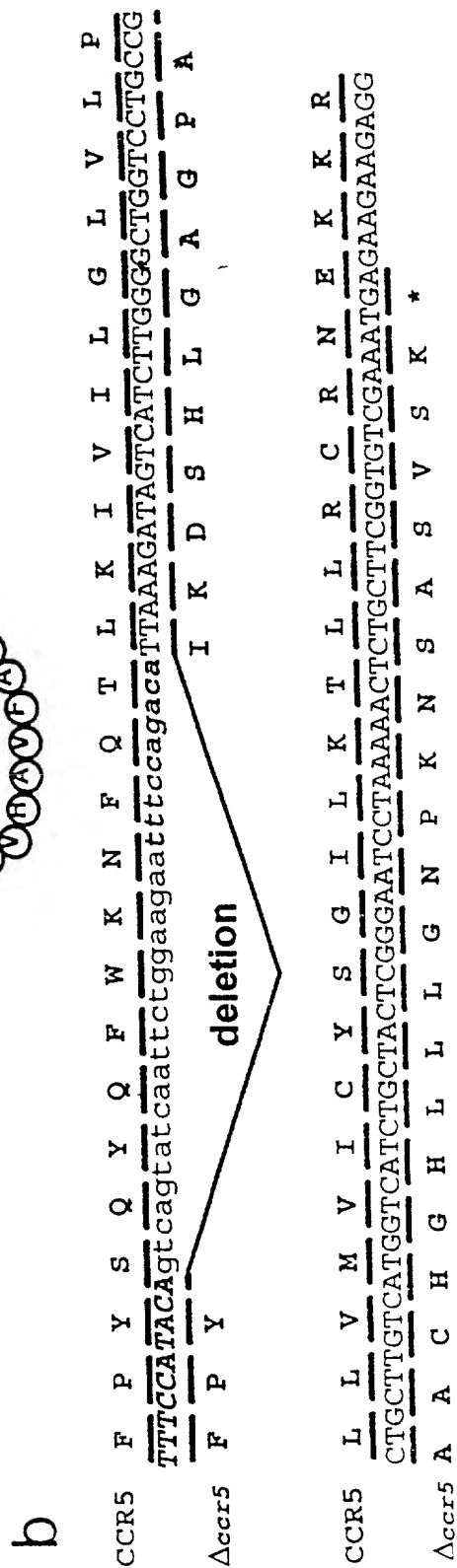


FIG. 6



A.

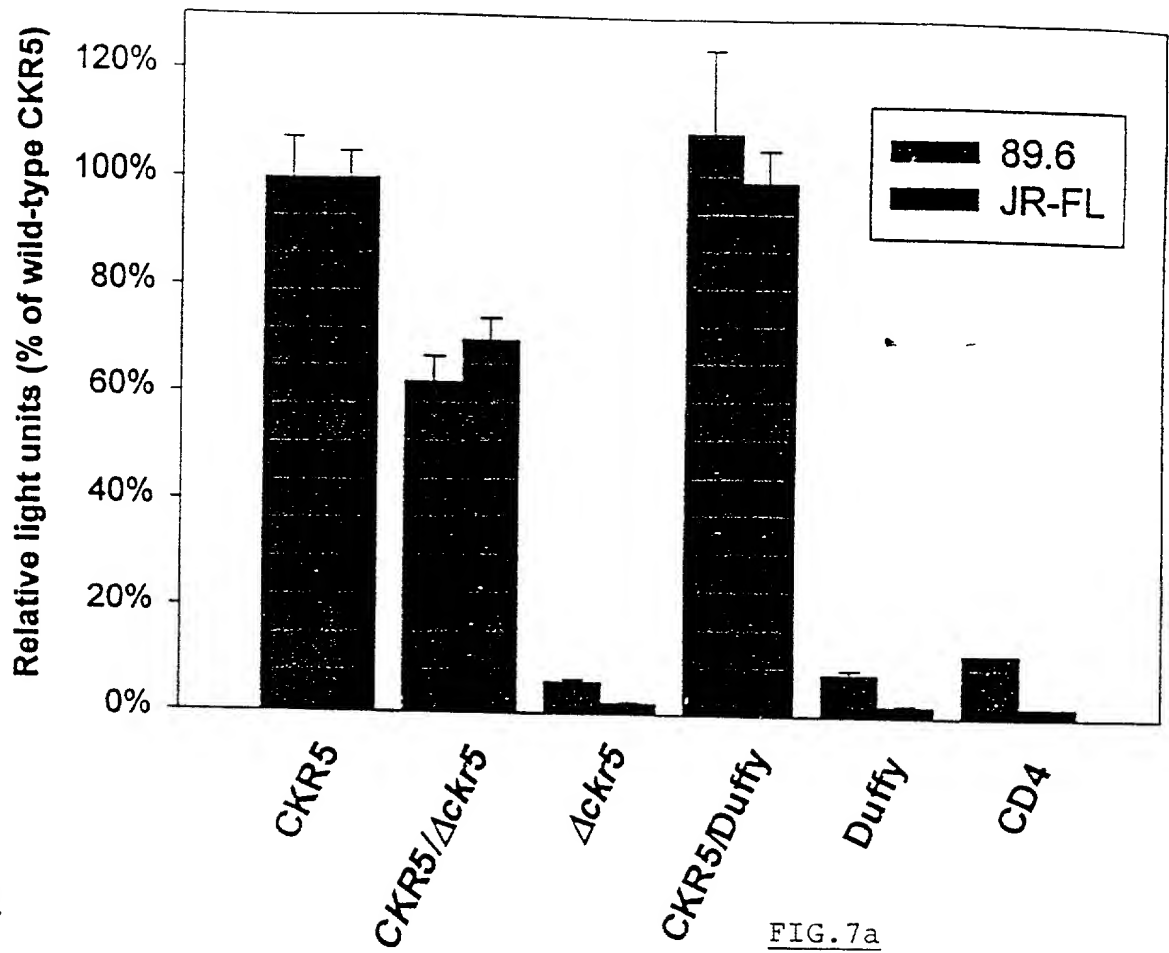


FIG. 7a

B.

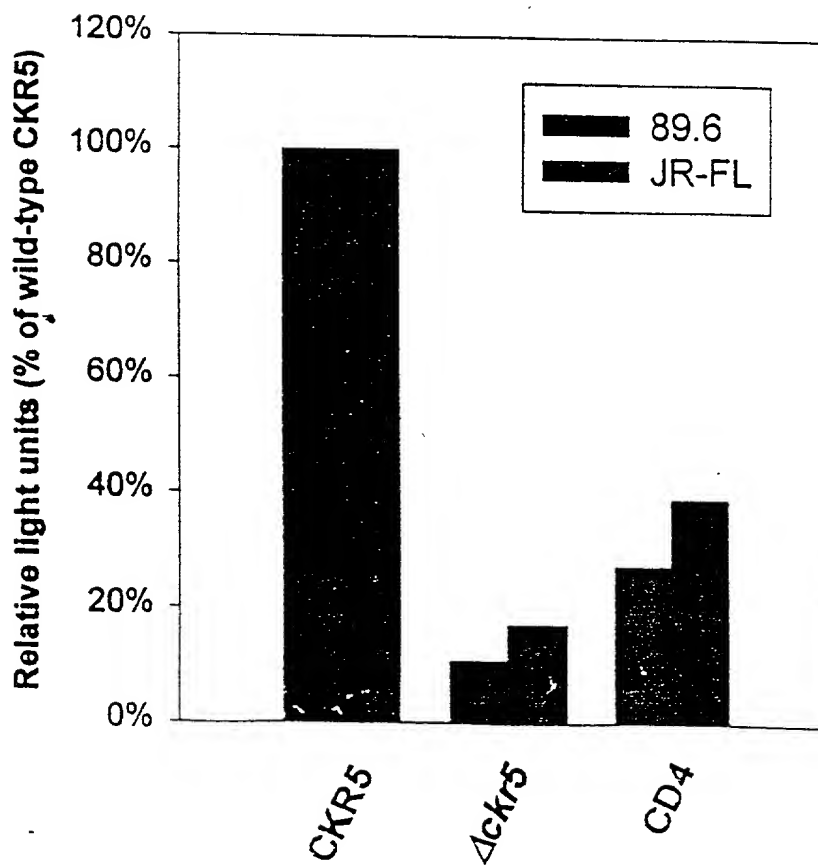


FIG. 7b

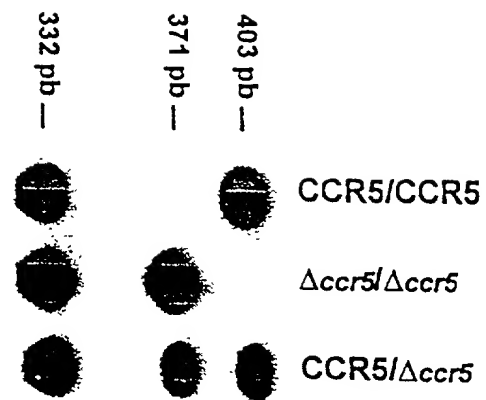


FIG. 8

09939226 082401

099999.03401

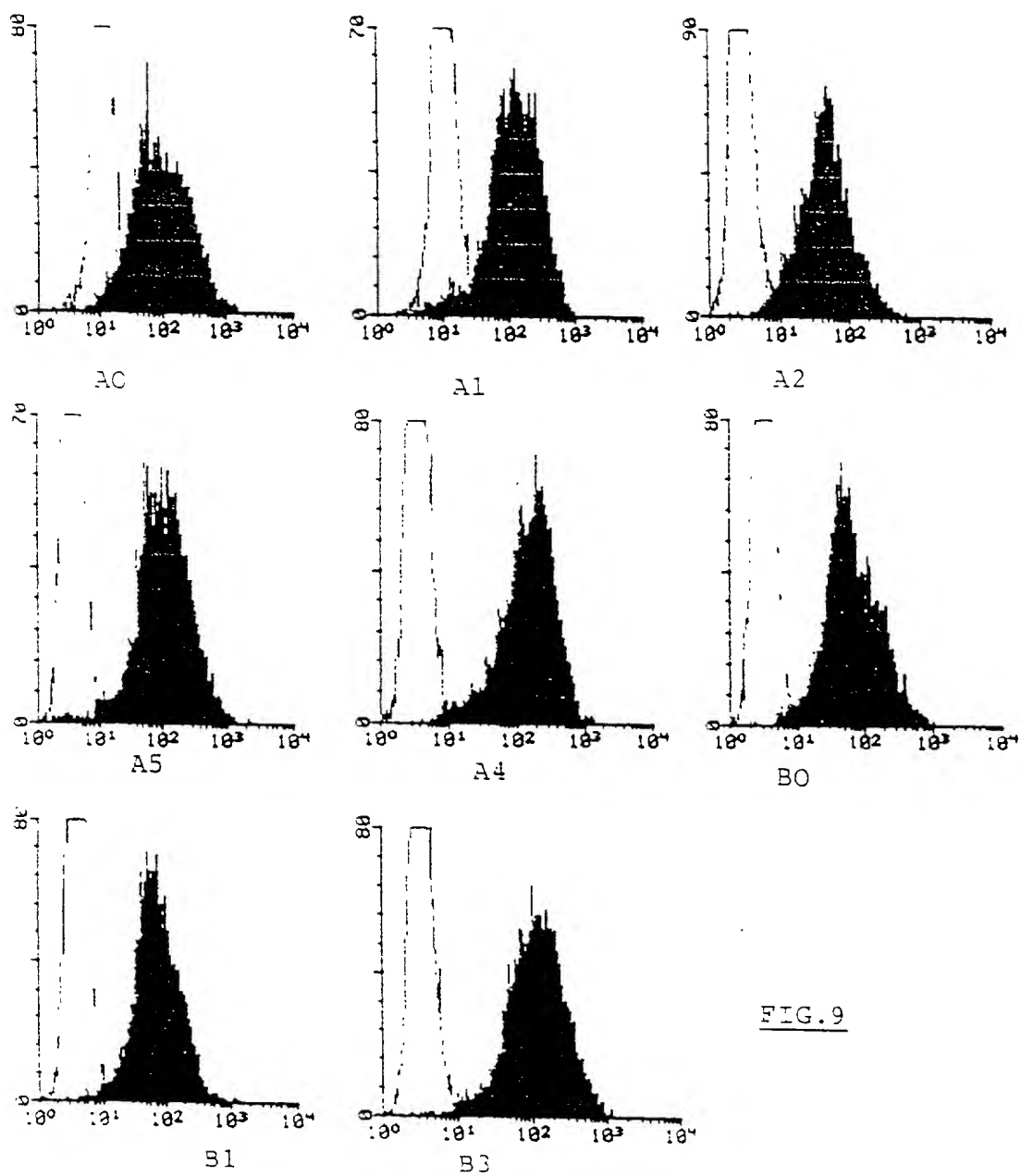


FIG.9

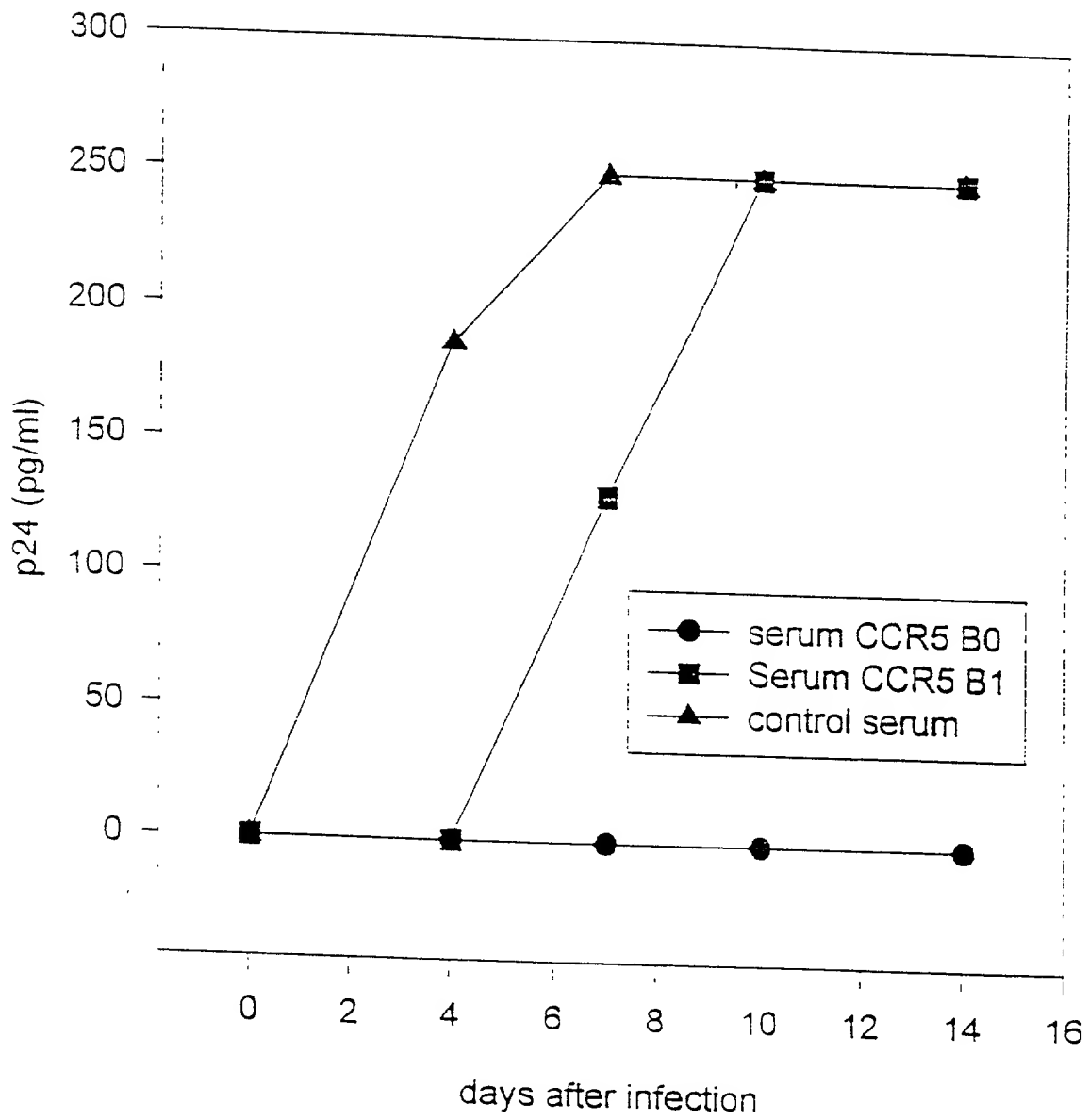


FIG.10